

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/509,954
Source: Pg 110
Date Processed by STIC: 1/9/06

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PCT

RAW SEQUENCE LISTING

DATE: 01/09/2006

PATENT APPLICATION: US/10/509,954

TIME: 11:22:12

Input Set : A:\32436ASEQLIST.TXT

Output Set: N:\CRF4\01092006\J509954.raw

```

4 <110> APPLICANT: Barclay, Jane
5      Buxton, Francis Paul
6      Ganju, Pamposh
7      Natt, Francois Jean-Charles
8      Song, Chuanzheng
9      Weiler, Jan
10     Wishart, William Leonard
12 <120> TITLE OF INVENTION: Use of MOB-5 in Pain
15 <130> FILE REFERENCE: PN/4-32436A
17 <140> CURRENT APPLICATION NUMBER: 10/509,954
18 <141> CURRENT FILING DATE: 2004-10-04
20 <150> PRIOR APPLICATION NUMBER: PCT/EP03/03469
21 <151> PRIOR FILING DATE: 2003-04-02
23 <150> PRIOR APPLICATION NUMBER: 60/369,893
24 <151> PRIOR FILING DATE: 2002-04-03
26 <160> NUMBER OF SEQ ID NOS: 20
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 29
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Primer Sequences for Rat MOB-5 gene
38 <400> SEQUENCE: 1
39 atgcagacaa gcttgagaca acagattct 29
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 27
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: Primer Sequences for Rat MOB-5 gene
49 <400> SEQUENCE: 2
50 tcagagctgg tagaaattct gcatcca 27
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 393
54 <212> TYPE: DNA
55 <213> ORGANISM: Rattus
57 <220> FEATURE:
58 <221> NAME/KEY: prim_transcript
59 <222> LOCATION: (28)...(48)
60 <223> OTHER INFORMATION: Gene Specific Primer Sequence designed from Rat
61     MOB-5 gene
63 <221> NAME/KEY: prim_transcript

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64 <222> LOCATION: (175)...(198)
65 <223> OTHER INFORMATION: Gene Specific Primer Sequence designed from Rat
66     MOB-5 gene
W--> 68 <400> 3
69 cttgattgcc aatccggata acttcctcct ttgttctccg tgccatttca aggcattgtt 60
70 catatccctg ttgtcctcag ggcacttcag acccttggcc atggaccctt gtcgttggct 120
71 caggcttttc ttcagacctc actctttagt ccaaacgaca gccatggaca gcaccttgg 180
72 atgctccgac tgaccacaaa cgtggatttg catatttatt acagccctat ttaactaatg 240
73 tcaactgtttc ggtagaaacc ggtatttatt tgtgagactg gacgttccat gaaagcatca 300
74 tgccccgtgt ttgcacctta cttcctgtga gctggctcac catgggggca gtagatggtt 360
75 gctcagtaaa tatttaaaat ggaaaaaaaaaaa aaa 393
77 <210> SEQ ID NO: 4
78 <211> LENGTH: 21
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: RT-PCR Primer region for rat MOB-5 gene
85 <400> SEQUENCE: 4
86 cctttgttct ccgtgccatt t 21
88 <210> SEQ ID NO: 5
89 <211> LENGTH: 23
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: RT-PCR Primer region for rat MOB-5 geneMOB-5 gene
96 <400> SEQUENCE: 5
97 ctttggatgc tccgactgac cca 23
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 183
101 <212> TYPE: PRT
102 <213> ORGANISM: Rattus
104 <220> FEATURE:
105 <221> NAME/KEY: PEPTIDE
106 <222> LOCATION: (1)...(183)
107 <223> OTHER INFORMATION: Amino Acid sequence corresponding to the Open
108     Reading Frame region deduced from MOB-5 cDNAs
109     Cloned from Rattus Dorsal Root Ganglia
111 <400> SEQUENCE: 6
112 Met Gln Thr Ser Leu Arg Gln Gln Ile Leu Pro Gly Leu Ser Leu Ile
113 1 5 10 15
114 Leu Leu Val Leu Ser Gln Val Pro Glu Leu Gln Gly Gln Glu Phe Arg
115 20 25 30
116 Phe Gly Pro Cys Gln Val Thr Gly Val Val Leu Pro Glu Leu Trp Glu
117 35 40 45
118 Ala Phe Trp Thr Val Lys Asn Thr Val Lys Thr Gln Asp Glu Leu Thr
119 50 55 60
120 Ser Val Arg Leu Leu Lys Pro Gln Val Leu Gln Asn Val Ser Asp Ala
121 65 70 75 80
122 Glu Ser Cys Tyr Leu Ala His Ser Leu Leu Lys Phe Tyr Leu Asn Thr

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123          85          90          95
124 Val Phe Lys Asn Tyr His Ser Glu Ile Val Lys Phe Lys Val Leu Lys
125          100          105          110
126 Ser Phe Ser Thr Leu Ala Asn Asn Phe Leu Val Ile Met Ser Lys Leu
127          115          120          125
128 Gln Pro Ser Lys Asp Asn Ala Met Leu Pro Ile Ser Asp Ser Ala Arg
129          130          135          140
130 Arg Arg Phe Leu Leu Phe His Arg Thr Phe Lys Gln Leu Asp Ile Glu
131 145          150          155          160
132 Val Ala Leu Ala Lys Ala Phe Gly Glu Val Asp Ile Leu Leu Ala Trp
133          165          170          175
134 Met Gln Asn Phe Tyr Gln Leu
135          180
138 <210> SEQ ID NO: 7
139 <211> LENGTH: 18
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Antisense Oligonucleotide
W--> 146 <221> NAME/KEY: modified_base
147 <222> LOCATION: 1-5, 14-18
148 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl)
W--> 150 <221> modified_base
151 <222> LOCATION: 6-13
152 <223> OTHER INFORMATION: modified with a phosphorothioate group
W--> 154 <221> modified_base
155 <222> LOCATION: 2,5,16
156 <223> OTHER INFORMATION: m5c
W--> 158 <400> 7
159 tcagcaggct gtgggcaa 18
161 <210> SEQ ID NO: 8
162 <211> LENGTH: 18
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Antisense Oligonucleotide
W--> 169 <221> NAME/KEY: modified_base
170 <222> LOCATION: 1-5, 14-18
171 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group
W--> 173 <221> modified_base
174 <222> LOCATION: 6-13
175 <223> OTHER INFORMATION: modified with phosphorothioate group
W--> 177 <221> modified_base
178 <222> LOCATION: 2-3, 16
179 <223> OTHER INFORMATION: m5c
W--> 181 <400> 8
182 tccgaaggcg gtgtgcaa 18
184 <210> SEQ ID NO: 9
185 <211> LENGTH: 18

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186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: Antisense oligonucleotide
W--> 192 <221> NAME/KEY: modified_base
193 <222> LOCATION: 1-5, 14-18
194 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group
W--> 196 <221> modified_base
197 <222> LOCATION: 2,5, 16
198 <223> OTHER INFORMATION: m5c
W--> 200 <400> 9
201 tcagcaggct gtgggcaa 18
203 <210> SEQ ID NO: 10
204 <211> LENGTH: 18
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Antisense oligonucleotide
W--> 211 <221> NAME/KEY: modified_base
212 <222> LOCATION: 1-5, 14-18
213 <223> OTHER INFORMATION: modified with 2'-O-(2-methoxyethyl) group
W--> 215 <221> modified_base
216 <222> LOCATION: 2,3, 16
217 <223> OTHER INFORMATION: m5c
W--> 219 <400> 10
220 tccgaaggcg gtgtgcaa 18
222 <210> SEQ ID NO: 11
223 <211> LENGTH: 549
224 <212> TYPE: DNA
225 <213> ORGANISM: Rattus
227 <220> FEATURE:
228 <221> NAME/KEY: gene
229 <222> LOCATION: (1)...(549)
230 <223> OTHER INFORMATION: Rat MOB-5 cDNA
232 <400> SEQUENCE: 11
233 atgcagacaa gcttgagaca acagattctc cccggcctga gcctaatacct tctcgttttg 60
234 agccaagtac cagagcttca ggggtcaagag ttccgatttg ggctttgcca agtgaccggg 120
235 gtggttctcc cagaactgtg ggaggccttc tggactgtga agaacactgt gaaaactcag 180
236 gacgagctca caagtgtccg gctgttgaaa ccacaggttc tgcagaatgt ctcgatgcc 240
237 gagagctgtt accttgccca cagcctgctg aagttctact tgaacactgt tttcaaaaac 300
238 tatcacagcg aaatagtcaa attcaaggtc ttgaagtcac tctccactct ggccaacaac 360
239 ttttttagtca tcatgtccaa actgcagcct agtaaggaca atgccatgct tcccattagt 420
240 gacagtgcac gccggcgttt tttgctgttc cacagaacat tcaaacagtt ggacatagaa 480
241 gtggcttttg cgaaagcctt tgggggaagtg gacattctcc tggcctggat gcagaatttc 540
242 taccagctc 549
244 <210> SEQ ID NO: 12
245 <211> LENGTH: 21
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence

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249 <220> FEATURE:
250 <223> OTHER INFORMATION: Antisense Oligoribonucleotides sequence to rat
251     MOB-5 gene
W--> 253 <221> NAME/KEY: modified_base
254 <222> LOCATION: 1-18
255 <223> OTHER INFORMATION: phosphodiester internucleotide linkage
W--> 257 <221> modified_base
258 <222> LOCATION: 19-21
259 <223> OTHER INFORMATION: deoxyribonucleoside internucleotide linkage
W--> 261 <400> 12
262 uucagcaggc ugugggcaag g                                21
264 <210> SEQ ID NO: 13
265 <211> LENGTH: 21
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Sense Oligoribonucleotides sequence to rat MOB-5
271     gene
W--> 273 <221> NAME/KEY: modified_base
274 <222> LOCATION: 1-18
275 <223> OTHER INFORMATION: phosphodiester internucleotide linnkage
W--> 277 <221> modified_base
278 <222> LOCATION: 19-21
279 <223> OTHER INFORMATION: deoxyribobnucleoside internucleotide linkagechm5u
W--> 281 <400> 13
282 uugcccacag ccugcugaat t                                21
284 <210> SEQ ID NO: 14
285 <211> LENGTH: 21
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Mismatch Antisense Oligoribonucleotides to rat
291     MOB-5 gene
W--> 293 <221> NAME/KEY: modified_base
294 <222> LOCATION: 1-18
295 <223> OTHER INFORMATION: phosphodiester internucleotide linkages
W--> 297 <221> modified_base
298 <222> LOCATION: 19-21
299 <223> OTHER INFORMATION: deoxyribose internucleotide linages
W--> 301 <400> 14
302 uuccgaaggc ggugugcaag g                                21
304 <210> SEQ ID NO: 15
305 <211> LENGTH: 21
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Mismatch Sense oligoribonucleotides to rat MOB-5
311     gene
W--> 313 <221> NAME/KEY: modified_base

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VERIFICATION SUMMARY

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Input Set : A:\32436ASEQLIST.TXT

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L:68 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:146 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:150 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:154 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:158 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:169 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:181 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:192 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:196 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:200 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:211 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:215 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:219 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:253 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:257 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:261 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:273 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:277 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:281 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
L:293 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:297 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:301 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:313 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:317 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:321 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:333 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:337 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:341 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:353 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:357 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:361 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:373 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:377 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
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L:393 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:397 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:401 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:413 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:417 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20